



Sequence Revision History

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Revision history for "AF027217"			
GI	Version	Update Date	Status
2689645	1	Sep 24 1998 17:14	Live
2689645	1	May 14 1998 13:09	Dead
2689645	1	Dec 17 1997 0:15	Dead

Accession AF027217 was first seen at NCBI on Dec 17 1997 0:15

Revised: July 5, 2002.

Revised: July 5, 2002.

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Mar 17 2003 10:55:57



**Nucleotide**

PubMed

**Nucleotide**

Protein

## Genome

## Structure

PMC

## Taxonomy

OMIM

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## Limits

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## History

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## Details

Display: default Show: 20 Send to: File Get Subsequence

1: AF027217. Porcine circoviru...[qi:2689645]

## Links

```

LOCUS      AF027217          1768bp    DNA      circular VRL 14-MAY-1998
DEFINITION Porcine circovirus strain pmws PCV, complete genome.
ACCESSION  AF027217
VERSION    AF027217.1  GI:2689645
KEYWORDS   .
SOURCE     Porcine circovirus
  ORGANISM Porcine circovirus
            Viruses; ssDNA viruses; Circoviridae; Circovirus.
REFERENCE  1  (bases 1 to 1768)
  AUTHORS  Hamel,A.L., Lin,L.L. and Nayar,G.P.
  TITLE    Nucleotide sequence of porcine circovirus associated with
            postweaning multisystemic wasting syndrome in pigs
  JOURNAL   J. Virol. 72 (6), 5262-5267 (1998)
  MEDLINE   98241772
  PUBMED    9573301
REFERENCE  2  (bases 1 to 1768)
  AUTHORS  Hamel,A.L., Lin,L.L. and Nayar,G.P.S.
  TITLE    Direct Submission
  JOURNAL   Submitted (26-SEP-1997) Virology Laboratory, Veterinary Services
            Branch, Manitoba Agriculture, 545 University Crescent, Winnipeg,
            Manitoba R3T 5S6, Canada
FEATURES   Location/Qualifiers
     source          1..1768
                     /organism="Porcine circovirus"
                     /strain="pmws PCV"
                     /db_xref="taxon:46221"
                     /note="both strands of seven overlapping PCR fragments
                     were sequenced; virus isolated from lung, lymph node,
                     spleen and tonsil tissue from pigs affected by post
                     weaning multisystemic wasting syndrome"
     CDS           complement(join(1732..1768,1..92))
                     /note="ORF9; predicted 4.6 kDa protein"
                     /codon_start=1
                     /protein_id="AAC59470.1"
                     /db_xref="GI:2689654"
                     /translation="MWLGSA SILLAGHVAAEVLPRCCRCRSALVILTAHFFRFQL"
     stem_loop    join(1746..1768,1..13)
                     /function="putative replication site"
     rep_origin   join(1762..1768,1..2)
                     /note="'AAGTATTAC' is similar to the nonanucleotide motif
                     in the non-pathogenic PCV, GenBank Accession Number
                     U49186"
     CDS           51..995
                     /note="ORF1; similar to Rep protein encoded by
                     non-pathogenic PCV, GenBank Accession Number U49186;
                     predicted 35.8 kDa protein"

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/protein\_id="AAC59462.1"  
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QKRDWKTNVHVIVGPPGCGKSKWAANFADPETTYWKPPRNKWWWDGYHGEEVVVIDDFY  
GWLPWDDLLRLCDRYPLTVETKGGTVPFLARSILITSNQTPLEWYSSTAVPAVEALYR  
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misc feature 117..125  
/note="glycosylation site"

misc feature 816..824  
/note="glycosylation site"

misc feature 906..914  
/note="glycosylation site"

polyA signal 327..332  
CDS complement(357..671)  
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CDS complement(386..565)  
/note="ORF4; predicted 6.5 kDa protein"  
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/db\_xref="GI:2689649"  
/translation="MTCTLVFQSRFCIFPLTFKSSASPRKFLTNVTGCCSATVTRLPL  
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misc feature complement(470..478)  
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CDS complement(688..753)  
/note="ORF8; predicted 2.3 kDa protein"  
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/db\_xref="GI:2689653"  
/translation="MDIDHTVSVDHPTAASHKSHQ"

polyA signal 983..988  
CDS complement(989..1033)  
/note="ORF11; predicted 1.8 kDa protein"  
/codon\_start=1  
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/db\_xref="GI:2689656"  
/translation="MKNKNHYEVIKKTQ"

CDS 1016..1177  
/note="ORF5; predicted 6.2 kDa protein"  
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CDS complement(1034..1735)  
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misc feature

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CDS

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CDS

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/note="ORF10; predicted 4.1 kDa protein"  
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CDS

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BASE COUNT      452 a      360 c      495 g      461 t  
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1621 tccaacggta gcggtggcgg ggggtggacga gccaggggag gcggcgagg atctggccaa
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1741 aaaacgaaag aagthcgctg taagtatt
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//